

SEQUENCE LISTING

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(1) GENERAL INFORMATION:

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(i) APPLICANT:

- (A) NAME: Boehringer Ingelheim International GmbH
- (B) STREET: Binger Strasse 173
- (C) CITY: Ingelheim am Rhein
- (E) COUNTRY: Germany
- (F) POSTAL CODE (ZIP): 55216
- (G) TELEPHONE: 06132/772282
- (H) TELEFAX: 06132/774377

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(ii) TITLE OF INVENTION: Tumor-associated Antigen

(iii) NUMBER OF SEQUENCES: 28

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(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA to mRNA

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(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

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(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homo sapiens
- (F) TISSUE TYPE: Melanoma

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(ix) FEATURE:

- (A) NAME/KEY: 3'UTR

(B) LOCATION:340..679

(ix) FEATURE:

5 (A) NAME/KEY: 5'UTR
(B) LOCATION:1..9

(ix) FEATURE:

10 (A) NAME/KEY: CDS
(B) LOCATION:10..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

15	CGA GGG GCG ATG CTG ATG GGC CAG GAG GGC CTG GCA TTC CTG ATG GGC	48
	Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala	
	1 5 10	
20	CAG GGG GCA ATG CTG GCG GGC CAG GAG AGG CCG GTG CCA CCG GCG GCA	96
	Gln Gly Ala Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala	
	15 20 25	
25	GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG CCT CCG GGC CCA GAG GAG	144
	Glu Val Pro Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu	
	30 35 40 45	
30	GCG CCC CCG GGG GTC CCG ATG GCG GTG CCG CTT CTG CCG AGG ATG GAA	192
	Ala Pro Arg Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu	
	50 55 60	
35	GGT GGC CCT GCG GGG CCA GGA GGC CCG ACA GGC GGC TGC TTC AGT TGC	240
	Gly Ala Pro Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys	
	65 70 75	
40	ACA TCA CGA TGC CTT TCT OGT CCG CCA TGG AAG CCG AGC TGG TCC GCA	288
	Thr Ser Arg Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala	
	80 85 90	
45	GGA TCC TGT CCC GGG ATG CCG CAC CTC TCC CCC GAC CAG GGG CCG TTC	336
	Gly Ser Cys Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe	
	95 100 105	
50	TGA AGGACTTCAC CGTGTCGGC AACCTACTGT TTATCCGACT GACTGCTGCA	389
	*	
55	110	
	GACCAACGGC AACTGCAGCT CTCATCAGC TCTGTCTCC AGCAGCTTTC CCTGTGATG	449
	TGGATCAAGC AGTGCTTTCT GCGGTGTTT TTGGCTCAGG CTCCTCAGG GCAGAGGCGC	509
	TAAGCCAGC CTGGGCGCCC TTCTAGGTTC ATGCTCTCTC CCTAGGGGAA TGGTCCAGC	569
	ACGAGTGGC AGTTCAATTGT GGGGGCTGA TTGTTGTGCG CTGGAGGAGG ACGGCTTACA	629
	TGTTGTGTTT TGTAGAAAT AAAGCTGAGC TACGAAAAA AAAAAAAAAA	679

(2) INFORMATION FOR SEQ ID NO: 2:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

15 Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala
 1 5 10 15

Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro
 20 25 30

20 Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg
 35 40 45

Gly Val Arg Met Ala Val Pro Leu Leu Arg Arg Met Glu Gly Ala Pro
 50 55 60

25 Ala Gly Pro Gly Gly Arg Thr Ala Ala Cys Phe Ser Cys Thr Ser Arg
 65 70 75 80

30 Cys Leu Ser Arg Arg Pro Trp Lys Arg Ser Trp Ser Ala Gly Ser Cys
 85 90 95

Pro Gly Met Pro His Leu Ser Pro Asp Gln Gly Arg Phe *
 100 105 110

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(2) INFORMATION FOR SEQ ID NO: 3:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 767 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

50 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homo sapiens
 (F) TISSUE TYPE: Melanoma

55 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 54...596

(ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION:597..767

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(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION:1..53

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

15	ATCTCTGGTGG GCGCTGAOCT TCCTCTCTGAG AGCGGGGAG AGGCTOOGGA GGC ATG	56
	Met	
	1	
20	CAG GGC GAA GGC CAG GGC ACA GGG GGT TOG ACG GGC GAT GCT GAT GGC	104
	Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
	5 10 15	
25	CCA GGA GGC OCT GGC ATT OCT GAT GGC CCA GGG GGC AAT GCT GGC GGC	152
	Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
	20 25 30	
30	CCA GGA GAG GCG GGT GGC ACG GGC GGC AGA GGT CCG CCG GGC GCA GGG	200
	Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
	35 40 45	
35	GCA GCA AGG GGC TOG GGG CCG AGA GGA GGC GGC CCG CCG GGT CCG CAT	248
	Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
	50 55 60 65	
40	GGC GGT GGC GCT TCT GCG CAG GAT GGA AGG TGC CCG TGC GGG GGC AGG	296
	Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	
	70 75 80	
45	AGG CCG GAC AGC CCG CTG CTT CAG TTG CAC ATC ACG ATG OCT TTC TOG	344
	Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	
	85 90 95	
50	TOG CCG ATG GAA GCG GAG CTG GTC CCG AGG ATC CTG TOC CCG GAT GGC	392
	Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	
	100 105 110	
55	GCA OCT CTC CCG CCA CCA GGG GCG GTT CTG AAG GAC TTC ACC GTG TOC	440
	Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	
	115 120 125	
50	GGC AAC CTA CTG TTT ATC CCA CTG ACT GCT GCA GAC CAC CCG CAA CTG	488
	Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu	
	130 135 140 145	
55	CAG CTC TOC ATC AGC TOC TGT CTC CAG CAG CTT TOC CTG TTG ATG TGG	536
	Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp	
	150 155 160	

ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG GCT CCC TCA GGG 584
 Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser Gly
 165 170 175

5 CAG AGG CGC TAA GGCAGGCTG GGGGGGCTC CTAGGTCATG CCTCTCTCCC 636
 Gln Arg Arg *
 180

10 TAGGGAATGG TOCCAGCAAG AGTGGCCAGT TCATTGTGGG GGCTGATTG TTGTGCGCTG 696
 GAGGAGGACG GCTTACATGT TTGTTCTGT AGAAAATAAA GCTGAGCTAC GAAAAAAAAA 756
 AAAAAAAAAA A 767

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(2) INFORMATION FOR SEQ ID NO: 4:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

30 Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp 15
 1 5 10 15
 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly 30
 20 25 30
 35 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala 45
 35 40 45
 Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro 60
 40 50 55 60
 His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala 80
 65 70 75 80
 45 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe 95
 85 90 95
 Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp 110
 100 105 110
 50 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val 125
 115 120 125
 Ser Gly Asn Leu Leu Phe Ile Arg Leu Thr Ala Ala Asp His Arg Gln 140
 130 135 140
 55 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met 160
 145 150 155 160

6/18

Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Ala Pro Ser
 165 170 175

5 Gly Gln Arg Arg *
 180

(2) INFORMATION FOR SEQ ID NO: 5:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

20

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

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- (A) ORGANISM: homo sapiens
 (F) TISSUE TYPE: Melanoma

(ix) FEATURE:

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- (A) NAME/KEY: 5'UTR
 (B) LOCATION:1..55

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION:56..688

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(ix) FEATURE:

- (A) NAME/KEY: 3'UTR
 (B) LOCATION:689..993

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

	GCATCTCTGT GGGGCTGAC CTCTCTCTG AGAGCGGGC AGAGGCTG GAGC ATG	58
		Met
		1
45	CAG GGC GAA GGC CAG GGC ACA GGC GGT TOG ACG GGC GAT GCT GAT GGC	106
	Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly	
	5 10 15	
50	CCA GGA GGC OCT GGC ATT OCT GAT GGC CCA GGC GGC AAT GCT GGC GGC	154
	Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly	
	20 25 30	
55	CCA GGA GAG GCG GGT GGC ACG GGC GGC AGA GGT CCG CCG GGC CCA GGC	202
	Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly	
	35 40 45	
	GCA GCA AGG GGC TOG GGC CCG AGA GGA GGC GGC CCG CCG GGT CCG CAT	250

	Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro His	
	50 55 60 65	
5	GGC GGT GGC GCT TCT GCG CAG GAT GGA AGG TGC CCC TGC GGG GGC AGG Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala Arg	298
	70 75 80	
10	AGG CCG GAC AGC CCG CTG CTT CAG TTG CAC ATC ACG ATG OCT TTC TCG Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe Ser	346
	85 90 95	
15	TCG CCC ATG GAA GCG GAG CTG GTC CCG AGG ATC CTG TCC CCG GAT GGC Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp Ala	394
	100 105 110	
20	GCA OCT CTC CCC CGA CCA GCG GCG GTT CTG AAG GAC TTC ACC GTG TCC Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val Ser	442
	115 120 125	
25	GGC AAC CTA CTG TTT ATG TCA GTT CCG GAC CAG GAC AGG GAA GGC GCT Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly Ala	490
	130 135 140 145	
30	GGG CCG ATG AGG GTG GTG GGT TGG GCG CTG GGA TCC GGC TCC CCG GAG Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro Glu	538*
	150 155 160	
35	GGG CAG AAA GCT AGA GAT CTC AGA ACA CCC AAA CAC AAG GTC TCA GAA Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser Glu	586
	165 170 175	
40	CAG AGA OCT GGT ACA CCA GCG CCG CCG CCA CCC GAG GGA GGC CAG GGA Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln Gly	634
	180 185 190	
45	GAT GGG TGC AGA GGT GTC GGC TTT AAT GTG ATG TTC TCT GGC OCT CAC Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro His	682
	195 200 205	
50	ATT TAG CCGACTGACT GCTGCAGACC ACGGCCAACT GCAGCTCTCC ATCAGCTOCT Ile *	738
	210	
55	GCTCCAGCA GCTTTCCCTG TTGATGTGGA TCAGCAGTG CTTTCTGCCC GGTGTTTTGG	798
	CTCAGGCTCC CTCAGGCGAG AGGCGCTAAG CCGAGCCTGG CGCCCTCTCC TAGGTCATGC	858
	CTCCTCCCT AGGGAATGGT CCGACCAAGA GTGGCCAGTT CATTGTGGGG GCGTGATTGT	918
	TTGTGCTGG AGGAGCAAGG CTTACATGTT TGTTCCTGTA GAAAATAAAG CTGAGCTAAG	978
	AAAAAAAAA AAAAA	993

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

10 Met Gln Ala Glu Gly Gln Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
 1 5 10 15

Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
 20 25 30

15 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
 35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Arg Gly Gly Ala Pro Arg Gly Pro
 20 50 55 60

His Gly Gly Ala Ala Ser Ala Gln Asp Gly Arg Cys Pro Cys Gly Ala
 65 70 75 80

25 Arg Arg Pro Asp Ser Arg Leu Leu Gln Leu His Ile Thr Met Pro Phe
 85 90 95

Ser Ser Pro Met Glu Ala Glu Leu Val Arg Arg Ile Leu Ser Arg Asp
 100 105 110

30 Ala Ala Pro Leu Pro Arg Pro Gly Ala Val Leu Lys Asp Phe Thr Val
 115 120 125

Ser Gly Asn Leu Leu Phe Met Ser Val Arg Asp Gln Asp Arg Glu Gly
 35 130 135 140

Ala Gly Arg Met Arg Val Val Gly Trp Gly Leu Gly Ser Ala Ser Pro
 145 150 155 160

40 Glu Gly Gln Lys Ala Arg Asp Leu Arg Thr Pro Lys His Lys Val Ser
 165 170 175

Glu Gln Arg Pro Gly Thr Pro Gly Pro Pro Pro Pro Glu Gly Ala Gln
 180 185 190

45 Gly Asp Gly Cys Arg Gly Val Ala Phe Asn Val Met Phe Ser Ala Pro
 195 200 205

50 His Ile *
 210

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(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

9/18

(A) LENGTH: 752 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA to mRNA
(iii) HYPOTHETICAL: NO
10 (iv) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
15 (ix) FEATURE:
(A) NAME/KEY: 5'UTR
(B) LOCATION:1..53
(ix) FEATURE:
20 (A) NAME/KEY: CDS
(B) LOCATION:54..596
(ix) FEATURE:
25 (A) NAME/KEY: 3'UTR
(B) LOCATION:597..752
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

30 ATCTCTGTTGG GGGCTGACCT TCTCTCTGAG AGCGGGGAG AGGCTGCGGA GGC ATG 56
Met
1
CAG GGC GAA GGC CGG GGC ACA GGG GGT TCG ACG GGC GAT GCT GAT GGC 104
Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp Gly
5 10 15
CCA GGA GGC OCT GGC ATT OCT GAT GGC CCA GGC GGC AAT GCT GGC GGC 152
Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly Gly
20 25 30
CCA GGA GAG GCG GGT GGC ACG GGC GGC AGA GGT CCC CGG GGC GCA GGC 200
Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala Gly
35 40 45
GCA GCA AGG GGC TCG GGG CCG GGA GGA GGC GGC CCG CCG GGT CCG CAT 248
Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro His
50 55 60 65
GGC GGC GCG GCT TCA GGG CTG AAT GGA TGC TGC AGA TGC GGC GGC AGG 296
Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala Arg
70 75 80
GGG CCG GAG AGC CGC CTG CTT GAG TTC TAC CTC GGC ATG OCT TTC GGC 344
Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe Ala
85 90 95
ACA CCC ATG GAA GCA GAG CTG GGC CGC AGG ACC CTG GGC CAG GAT GGC 392

Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp Ala
 100 105 110

5 OCA CCG CTT CCC GTG CCA GGG GTG CTT CTG AAG GAG TTC ACT GTG TCC 440
 Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val Ser
 115 120 125

10 GGC AAC ATA CTG ACT ATC OGA CTG ACT GCT GCA GAC CAC CGC CAA CTG 488
 Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln Leu
 130 135 140 145

15 CAG CTC TCC ATC AGC TCC TGT CTC CAG CAG CTT TCC CTG TTG ATG TGG 536
 Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met Trp
 150 155 160

20 ATC ACG CAG TGC TTT CTG CCC GTG TTT TTG GCT CAG CCT CCC TCA GGG 584
 Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser Gly
 165 170 175

25 CAG AGG CGC TAA GGCAGCTG GGGCCCTTC CTAGGTCATG CCTCTCCCC 636
 Gln Arg Arg *
 180

30 TAGGGAATGG TCCAGCAG AGTGGCCAGT TCATTGTTGG GGCCTGATTG TTGTGCTG 696
 25 GAGGAGGAG GCTTACATGT TTGTTCTGT AGAAAATAAA ACTGAGCTAC GAAAAA 752

35 (2) INFORMATION FOR SEQ ID NO: 8:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 Met Gln Ala Glu Gly Arg Gly Thr Gly Gly Ser Thr Gly Asp Ala Asp
 1 5 10 15

45 Gly Pro Gly Gly Pro Gly Ile Pro Asp Gly Pro Gly Gly Asn Ala Gly
 20 25 30

50 Gly Pro Gly Glu Ala Gly Ala Thr Gly Gly Arg Gly Pro Arg Gly Ala
 35 40 45

Gly Ala Ala Arg Ala Ser Gly Pro Gly Gly Gly Ala Pro Arg Gly Pro
 50 55 60

55 His Gly Gly Ala Ala Ser Gly Leu Asn Gly Cys Cys Arg Cys Gly Ala
 65 70 75 80

Arg Gly Pro Glu Ser Arg Leu Leu Glu Phe Tyr Leu Ala Met Pro Phe
 85 90 95

Ala Thr Pro Met Glu Ala Glu Leu Ala Arg Arg Ser Leu Ala Gln Asp
 100 105 110

5 Ala Pro Pro Leu Pro Val Pro Gly Val Leu Leu Lys Glu Phe Thr Val
 115 120 125

Ser Gly Asn Ile Leu Thr Ile Arg Leu Thr Ala Ala Asp His Arg Gln
 130 135 140

10 Leu Gln Leu Ser Ile Ser Ser Cys Leu Gln Gln Leu Ser Leu Leu Met
 145 150 155 160

15 Trp Ile Thr Gln Cys Phe Leu Pro Val Phe Leu Ala Gln Pro Pro Ser
 165 170 175

Gly Gln Arg Arg *
 180

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(2) INFORMATION FOR SEQ ID NO: 9:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 752 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

35

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homo sapiens

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(ix) FEATURE:

(A) NAME/KEY: 5'UTR

(B) LOCATION:1..93

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(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION:94..270

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(ix) FEATURE:

(A) NAME/KEY: 3'UTR

(B) LOCATION:271..752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

55 ATCTCTGTGG GCGCTGACCT TCCTCTGAG AGCGGGGAG AGGCTCGGA GCGATGCAGG 60

CGGAGGCGG GGGCAGGG GGTTGAGGG GCG ATG CTG ATG GCG CAG GAG GCG 114

Met Leu Met Ala Gln Glu Ala

12/18

		1		5	
5	CTG GCA TTC CTG ATG GGC CAG GGG GCA ATG CTG GCG GGC CAG GAG AGG Leu Ala Phe Leu Met Ala Gln Gly Ala Met Leu Ala Ala Gln Glu Arg	162			
	10	15		20	
10	CGG GTG CCA CGG GCG GCA GAG GTC CCC GGG GCG CAG GGG CAG CAA GGG Arg Val Pro Arg Ala Ala Glu Val Pro Gly Ala Gln Gly Gln Gln Gly	210			
	25	30		35	
15	OCT CGG GGC CGG GAG GAG GCG CCC GCG GGG GTC GCG ATG GCG GCG CGG Pro Arg Gly Arg Glu Glu Ala Pro Arg Gly Val Arg Met Ala Ala Arg	258			
	40	45		50	55
20	CTT CAG GGC TGA ATGGATGCTG CAGATGCGGG GGCAGGGGGC CGGAGAGGCG Leu Gln Gly *	310			
25	CCCTCTTGAG TTCTAAGCTG CCATGCTTTT CGGACAAAC ATGGAAGCAG AGCTGGGCGG CAGGAGGCTG GGCAGGATG CCCCACCGCT TCCCGTGCCA GGGGTGCTTC TGAAGGAGTT	370			
	CACGTGTGCC GGCAACATAC TGAATATGCG ACTGACTGCT GCAGACCAAC GGCAGCTGCA	430			
30	GCCTTCATC AGCTCTGTC TCCAGCAGCT TTCCCTGTTG ATGTTGATCA CGCAGTGCTT TCTGCGGCTG TTTTGTGCTC AGCTCTGCTC AGGGCAGAGG CGCTAAGGCG AGCTGGGCGC	490			
	CCCTCTAG GTCATGCTC CTCCCTAGG GAATGGTCC AGCAAGAGTG GGCAGTTTAT	550			
35	TGTTGGGGGC TGATTTTGTG TCGCTGGAGG AGGACGGCTT ACATGTTTGT TTCGTAGAA AATAAACTG AGCTAAGAAA AA	610			
		670		730	752

(2) INFORMATION FOR SEQ ID NO: 10:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu Met Ala Gln Gly Ala
 1 5 10 15
 5 Met Leu Ala Ala Gln Glu Arg Arg Val Pro Arg Ala Ala Glu Val Pro
 20 25 30
 10 Gly Ala Gln Gly Gln Gln Gly Pro Arg Gly Arg Glu Glu Ala Pro Arg
 35 40 45
 Gly Val Arg Met Ala Ala Arg Leu Gln Gly *

15

2) INFORMATION FOR SEQ ID NO: 11:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 11 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

30 Met Leu Met Ala Gln Glu Ala Leu Ala Phe Leu
 1 5 10....

35 2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

45 Leu Met Ala Gln Glu Ala Leu Ala Phe Leu
 1 5 10.

50

(2) INFORMATION FOR SEQ ID NO: 13:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

5 GGTGACACTA TAGAAGGTAC G 21

10 (2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

20 TGATGTGCAA CTGAAGCAGG.....20

25 (2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

35 GCACTGGGTG ATCCACATCA A 21

40 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

50 CGACTCACTA TAGGTAGAGA G 21

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: synthetic DNA

GCACATCAAG ATGOCITTTCT CGTGG

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(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: synthetic DNA

CACACAAAGC TTGGCTTAGC GCCTCTGCCC TG.....32

30

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: synthetic DNA

CACACAGGAT CCATGGATGC TGCAGATGG.....30

45

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: synthetic DNA

GAAGAACATA TGCTGATGGC CCAGGAGGC

29

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

TTAAAGATCT CAGAACCGCC OCTGGTCG

28

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

ttactogaga tgctgatggc ccagg.....25

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

aaggtaacctt gaacogcccc tggtag26

2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Phe Leu Met Ala Gln Gly Ala Met Leu
1 5 9

5

2) INFORMATION FOR SEQ ID NO: 25:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

20 Ala Met Leu Ala Ala Gln Glu Arg Arg Val
1 5 10

25

2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

30

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Met Leu Ala Ala Gln Glu Arg Arg Val
1 5 9

40

2) INFORMATION FOR SEQ ID NO: 27:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

55 Tyr Tyr Met Asn Gly Thr Met Ser Gln Val
1 5 10

WO 00/23584

PCT/EP99/07832

18/18

2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Glu Val Asp Pro Ile Gly His Leu Tyr
1 5 9

15